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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/028,521

DATE: 01/16/2002

TIME: 18:32:55

Input Set : A:\-47-3.app

Output Set: N:\CRF3\01162002\J028521.raw

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MAR 20 2002
TC 1700

3 <110> APPLICANT: Powers, Scott
4 Yang, Jianxin
5 Cutler, Gene
6 Tularik Inc.
8 <120> TITLE OF INVENTION: Novel G-Protein Coupled Receptors
10 <130> FILE REFERENCE: 018781-004730US
12 <140> CURRENT APPLICATION NUMBER: US/10/028,521
13 <141> CURRENT FILING DATE: 2001-12-20
15 <150> PRIOR APPLICATION NUMBER: US 09/524,730
16 <151> PRIOR FILING DATE: 2000-03-14
18 <150> PRIOR APPLICATION NUMBER: US 09/546,986
19 <151> PRIOR FILING DATE: 2001-04-11
21 <160> NUMBER OF SEQ ID NOS: 23
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1035
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (42)..(974)
33 <223> OTHER INFORMATION: human breast cancer amplified G-protein coupled
34 receptor 1 (BCA-PCR-1)
36 <400> SEQUENCE: 1
37 agtgcagaa aatgccgcaa catgaaaagt gacaaccata g ctc tta ggg gac tcc 56
38 Leu Leu Gly Asp Ser
39 1 5
41 cct aaa gcc ttc atc ctt ctg ggt gtg tct gac agg ccg tgg ctg gaa 104
42 Pro Lys Ala Phe Ile Leu Leu Gly Val Ser Asp Arg Pro Trp Leu Glu
43 10 15 20
45 ctc cct ctc ttt gtg gtc ctc ctg ctg tcc tat gtg ctg gcc atg ttg 152
46 Leu Pro Leu Phe Val Val Leu Leu Leu Ser Tyr Val Leu Ala Met Leu
47 25 30 35
49 ggg aac gtc gcc atc atc ctg gca tcc cgg gtg gat cct caa ctc cac 200
50 Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val Asp Pro Gln Leu His
51 40 45 50
53 agc ccc atg tac atc ttc ctc agt cac ctg tcc ttc ctg gac ctc tgc 248
54 Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser Phe Leu Asp Leu Cys
55 55 60 65
57 tac acc acc acg aca gtc cct cag atg ctg gtc aac atg ggc agt tcc 296
58 Tyr Thr Thr Thr Thr Val Pro Gln Met Leu Val Asn Met Gly Ser Ser
59 70 75 80 85
61 cag aag acc atc agc tat gga ggc tgc act gtg caa tat gca gtc ttc 344

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62 Gln Lys Thr Ile Ser Tyr Gly Gly Cys Thr Val Gln Tyr Ala Val Phe
63          90          95          100
65 cac tgg ctg gga tgc acg gag tgc atc gtc ctg gcc gcc atg gcc ctg 392
66 His Trp Leu Gly Cys Thr Glu Cys Ile Val Leu Ala Ala Met Ala Leu
67          105          110          115
69 gac cgc tac gtg gcc agc tgc aag ccc ctg cac tat gcc gtt ctc atg 440
70 Asp Arg Tyr Val Ala Ser Cys Lys Pro Leu His Tyr Ala Val Leu Met
71          120          125          130
73 cac cgt gct ctc tgt cag cag ctc gtg gct ctg gcc tgg ctc agt ggc 488
74 His Arg Ala Leu Cys Gln Gln Leu Val Ala Leu Ala Trp Leu Ser Gly
75          135          140          145
77 ttc ggc aac tcc ttc gtg cag gtg gtc ctg acg gtg caa ttg cca ttc 536
78 Phe Gly Asn Ser Phe Val Gln Val Val Leu Thr Val Gln Leu Pro Phe
79 150          155          160          165
81 tgc ggg cgg cag gtg ctg aac aac ttt ttc tgt gag gtg ccg gcc gtg 584
82 Cys Gly Arg Gln Val Leu Asn Asn Phe Phe Cys Glu Val Pro Ala Val
83          170          175          180
85 atc aag ctg tcg tgt gct gac acc gct atg aat gac acc ata ctg gct 632
86 Ile Lys Leu Ser Cys Ala Asp Thr Ala Met Asn Asp Thr Ile Leu Ala
87          185          190          195
89 gtg ctg gtg gcc ttc ttc gtg ttg gtg ccc ctg gct ctc atc ctt ctc 680
90 Val Leu Val Ala Phe Phe Val Leu Val Pro Leu Ala Leu Ile Leu Leu
91          200          205          210
93 tcc tat ggc ttt att gcc cgg gca gtg ctc agg atc cag tcc tcc aag 728
94 Ser Tyr Gly Phe Ile Ala Arg Ala Val Leu Arg Ile Gln Ser Ser Lys
95          215          220          225
97 gga cga cac aag gcc ttt ggg acg tgt tcc tcc cac ctg atg atc gtc 776
98 Gly Arg His Lys Ala Phe Gly Thr Cys Ser Ser His Leu Met Ile Val
99 230          235          240          245
101 tcc ctc ttc tac cta cct gcg att tac atg tat ctg cag ccc cct tcc 824
102 Ser Leu Phe Tyr Leu Pro Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser
103          250          255          260
105 agc tac tcc caa gag cag ggc aaa ttt att tct ctc ttc tat tcc ata 872
106 Ser Tyr Ser Gln Glu Gln Gly Lys Phe Ile Ser Leu Phe Tyr Ser Ile
107          265          270          275
109 atc acc ccc act ctc aat ccc ttc acc tac acc ctg aga aat aaa gat 920
110 Ile Thr Pro Thr Leu Asn Pro Phe Thr Tyr Thr Leu Arg Asn Lys Asp
111          280          285          290
113 atg aag ggg gct ctg agg aga ctt ctg gcc agg atc tgg agg ctc tgt 968
114 Met Lys Gly Ala Leu Arg Arg Leu Leu Ala Arg Ile Trp Arg Leu Cys
115          295          300          305
117 gga tga tgaggacatg agatgtagca tctccatcaa ttaaagaaca cagcacaagt 1024
118 Gly
119 310
121 ctattgtgca c 1035
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 310
126 <212> TYPE: PRT
127 <213> ORGANISM: Homo sapiens

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129 <220> FEATURE:

130 <223> OTHER INFORMATION: human breast cancer amplified G-protein coupled

131 receptor 1 (BCA-GPCR-1)

133 <400> SEQUENCE: 2

134 Leu Leu Gly Asp Ser Pro Lys Ala Phe Ile Leu Leu Gly Val Ser Asp

135 1 5 10 15

136 Arg Pro Trp Leu Glu Leu Pro Leu Phe Val Val Leu Leu Leu Ser Tyr

137 20 25 30

138 Val Leu Ala Met Leu Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val

139 35 40 45

140 Asp Pro Gln Leu His Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser

141 50 55 60

142 Phe Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val Pro Gln Met Leu Val

143 65 70 75 80

144 Asn Met Gly Ser Ser Gln Lys Thr Ile Ser Tyr Gly Gly Cys Thr Val

145 85 90 95

146 Gln Tyr Ala Val Phe His Trp Leu Gly Cys Thr Glu Cys Ile Val Leu

147 100 105 110

148 Ala Ala Met Ala Leu Asp Arg Tyr Val Ala Ser Cys Lys Pro Leu His

149 115 120 125

150 Tyr Ala Val Leu Met His Arg Ala Leu Cys Gln Gln Leu Val Ala Leu

151 130 135 140

152 Ala Trp Leu Ser Gly Phe Gly Asn Ser Phe Val Gln Val Val Leu Thr

153 145 150 155 160

154 Val Gln Leu Pro Phe Cys Gly Arg Gln Val Leu Asn Asn Phe Phe Cys

155 165 170 175

156 Glu Val Pro Ala Val Ile Lys Leu Ser Cys Ala Asp Thr Ala Met Asn

157 180 185 190

158 Asp Thr Ile Leu Ala Val Leu Val Ala Phe Phe Val Leu Val Pro Leu

159 195 200 205

160 Ala Leu Ile Leu Leu Ser Tyr Gly Phe Ile Ala Arg Ala Val Leu Arg

161 210 215 220

162 Ile Gln Ser Ser Lys Gly Arg His Lys Ala Phe Gly Thr Cys Ser Ser

163 225 230 235 240

164 His Leu Met Ile Val Ser Leu Phe Tyr Leu Pro Ala Ile Tyr Met Tyr

165 245 250 255

166 Leu Gln Pro Pro Ser Ser Tyr Ser Gln Glu Gln Gly Lys Phe Ile Ser

167 260 265 270

168 Leu Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Pro Phe Thr Tyr Thr

169 275 280 285

170 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Arg Leu Leu Ala Arg

171 290 295 300

172 Ile Trp Arg Leu Cys Gly

173 305 310

176 <210> SEQ ID NO: 3

177 <211> LENGTH: 1411

178 <212> TYPE: DNA

179 <213> ORGANISM: Homo sapiens

181 <220> FEATURE:

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182 <221> NAME/KEY: CDS
183 <222> LOCATION: (118)..(1113)
184 <223> OTHER INFORMATION: human breast cancer amplified G-protein coupled
185      receptor 2 (BCA-GPCR-2)
187 <400> SEQUENCE: 3
188 ggcaaatggc tctcttaact tcacagacct gtaaatggaa attggagagt gccagatcat 60
190 ctgcatgtgc ccccttatct aattctttgg ttgtttctct gtaatagctg gtggatt 117
192 atg gga aag gac aat gcc agt tac cta cag gca ttc atc ctg gtg ggc 165
193 Met Gly Lys Asp Asn Ala Ser Tyr Leu Gln Ala Phe Ile Leu Val Gly
194   1           5           10           15
196 tct tct gat cgg cct gga ctg gag aaa att ctc ttt gct gtt atc ttg 213
197 Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
198           20           25           30
200 atc ttc tgc atc ctg acc ctg gtg ggc aac act gcc atc atc ctc ttg 261
201 Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
202           35           40           45
204 ctg gtc atg gat gtc agg ctc cac aca ccc atg tac ttc ttt ctt ggg 309
205 Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
206           50           55           60
208 aat ctg tct ttc tta gat ctc tgc ttt aca gca agc att gcc cct cag 357
209 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
210 65           70           75           80
212 ctg ctg tgg aac ctg ggg ggt cca gag aag acc atc acc tac cac ggc 405
213 Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
214           85           90           95
216 tgt gtg gcc caa ctc tac atc tac atg atg ctg ggc tcc acc gag tgc 453
217 Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
218           100          105          110
220 gtc ctc ctg gtt gtc atg tcc cat gac cgc tat gtg gcc gtc tgc cgg 501
221 Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
222           115          120          125
224 tcc ctg cac tac atg gca gtc atg cgc cca cat ctc tgc ctg cag ctg 549
225 Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
226           130          135          140
228 gtg act gtg gcc tgg tgc tgt ggc ttc cta aac tcc ttc atc atg tgt 597
229 Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
230 145          150          155          160
232 cct cag acg atg cag ctc tcc cgg tgt gga cgt cgc agg gtg gac cac 645
233 Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
234           165          170          175
236 ttc ctg tgt gag atg cct gct ctt att gcc atg tct tgt gag gaa acc 693
237 Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
238           180          185          190
240 atg ctg gta gaa gcg att cac ctt tgc cct ggg ggt ggc tct cct cct 741
241 Met Leu Val Glu Ala Ile His Leu Cys Pro Gly Gly Ser Pro Pro
242           195          200          205
244 ggt gcc gct ctc cct cat cct cat ctc tat ggc gtg att gca gcc gcg 789
245 Gly Ala Ala Leu Pro His Pro His Leu Tyr Gly Val Ile Ala Ala Ala
246           210          215          220

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248 gtg ctg agg atg aag tca gca gca ggg cga aag aaa gcc ttc cac acc 837
249 Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
250 225 230 235 240
252 tgc tct tct cac ctg aca gtg gtc tct ctg ttc tac gga acc atc atc 885
253 Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
254 245 250 255
256 tac gtg tac ctg aag ccg gcc aac agc tac tcc caa gat cag ggg aag 933
257 Tyr Val Tyr Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp Gln Gly Lys
258 260 265 270
260 ttc ctg act ctg ttc tac acc atc gtc att ccc agc atc aac ccc ctg 981
261 Phe Leu Thr Leu Phe Tyr Thr Ile Val Ile Pro Ser Ile Asn Pro Leu
262 275 280 285
264 atc tac act ttg agg aac aag gat gtg aag ggg acc atg aag aaa ctt 1029
265 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Thr Met Lys Lys Leu
266 290 295 300
268 ctg ggg tgg gag aaa ggg gct ggg gag cct caa cga ggg gaa cac tct 1077
269 Leu Gly Trp Glu Lys Gly Ala Gly Glu Pro Gln Arg Gly Glu His Ser
270 305 310 315 320
272 agt aat gta gac agt ttg ctg gag tta ctg tct tag atgtgtctgt 1123
273 Ser Asn Val Asp Ser Leu Leu Glu Leu Leu Ser
274 325 330
276 ggccatgtgg agaactaata ttcaaggagt agagtgaacg cgggtgggaa aatgctttcg 1183
278 agtttgaccc cgtcctctgc cctctggatg tgaagtgggt tccttctgtt tgaagttgcc 1243
280 tgcttcagga tatctctgct gtatcttgca ctttccttgt ctttttgatt tatccacaac 1303
282 tgctggggac ttacaaaact aattcaatca cccaaaggca ctgggcagtc tgcagattat 1363
284 gtcattgatg tcaataaaaa attgagacaa catgaaaaaa aaaaaaaa 1411
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 331
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <223> OTHER INFORMATION: human breast cancer amplified G-protein coupled
294 receptor 2 (BCA-GPCR-2)
296 <400> SEQUENCE: 4
297 Met Gly Lys Asp Asn Ala Ser Tyr Leu Gln Ala Phe Ile Leu Val Gly
298 1 5 10 15
299 Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
300 20 25 30
301 Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
302 35 40 45
303 Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
304 50 55 60
305 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
306 65 70 75 80
307 Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
308 85 90 95
309 Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
310 100 105 110
311 Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:606 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7